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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/079,699

DATE: 03/08/2002
TIME: 15:23:36

Input Set : A:\2104seq.txt
Output Set: N:\CRF3\03082002\J079699.raw

4 <110> APPLICANT: Nicholette, Charles A.
6 <120> TITLE OF INVENTION: PAR-3 COMPOUNDS FOR THERAPY AND DIAGNOSIS AND METHODS FOR
USING SAME
8 <130> FILE REFERENCE: GZ 2104.20
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/079,699
C--> 11 <141> CURRENT FILING DATE: 2002-02-19
13 <150> PRIOR APPLICATION NUMBER: 60/226,243
14 <151> PRIOR FILING DATE: 2000-08-17
16 <160> NUMBER OF SEQ ID NOS: 12
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 3801
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <400> SEQUENCE: 1
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27 atgaaagttt tcagcctcat ccagcaggcg gtgaccgcgt accggaaggc catgcctaag 120
28 gatccaaact actggataca ggtgcatcg tttggAACATG gagatggagg aataactagac 180
29 cttgtatgaca ttctttgtga ttagcagac gataaagaca gactggtagc agtgtttgat 240
30 gagcaggatc cacatcacgg aggtgtatggc accagtgcac gttccacggg taccagagc 300
31 ccagagatat ttggtagtga gcttggcacc aacaatgtct cagcctttca gccttaccaa 360
32 gcaacaagtg aaatttgaggt cacacccatca gtccttcgag caaatatgcc tcttcatgtt 420
33 cgacgcagta gtgaccccagc tctaattggc ctctccactt ctgtcagtgta tagtaatttt 480
34 tccttcgaag agccttcaag gaaaaatccc acacgttgtt caacaacagc tggcttcctc 540
35 aagcagaaca ctgctggag tctaaaacc tgcgacagga aggatgagga tgggacagaa 600
36 gaggataaca gtcgtgttga acctgttggc catgctgaca cgggtttgga gcatatacc 660
37 aacttttc tggatgat ggtaaagctc gtagaaatccc ccaacgtatgg agggctctg 720
38 ggaatccatg tagtgcctt cagtgtcga ggcggcagaa ccctggggtt attagtaaaa 780
39 cgattggaga aaggtggtaa agctgaacat gaaaatcttt ttcgtgagaa tgattgcatt 840
40 gtcaggatta atgatggcga ctttcgaaat agaagattt aacaaggcaca acatatgttt 900
41 cgccaagcca tgcgtacacc catcatttgg ttccatgtgg ttccctgcagc aaataaagag 960
42 cagtatgaac aactatccc aagtgagaag aacaattact attcaagccg ttttagccct 1020
43 gacagccagt atattgacaa caggagtgtg aacagtgcag gccttcacac ggtgcagaga 1080
44 gcaccccgac tgaaccaccc gcctgagcag atagactctc actcaagact acctcatagc 1140
45 gcacacccct cggaaaaacc accatccgcgt ccagcctcg cacctcagaa tgtatTTAGT 1200
46 acgactgtaa gcagtggta taacacccaa aaaataggca agaggcttaa tatccagctt 1260
47 aagaaaggta cagaaggttt gggattcagc atcacttcca gagatgtaac aataggtggc 1320
48 tcagctccaa tctatgtgaa aaacattctc cccccgggggg cggccattca ggtatggccga 1380
49 cttaaaggcag gagacagact tatagaggtt aatggagtag atttagtggg caaatcccaa 1440
50 gaggaagttt tttcgctgtt gagaaggcacc aagatggaaag gaactgtgag cttctggc 1500
51 tttcgccagg aagacgcctt ccacccaagg gaactgaaag cagaagatga ggtatTTAGT 1560
52 cttacacctg atggcaccag ggaatttctg acatttgaag tcccaactaa tgattcagga 1620
53 tctgcaggcc ttgggtgtcgt gtcgtaaagg aaccggcataa aagagaacca cgcagattt 1680
54 ggaatctttg tcaagtccat tattaatggg ggagcagcat ctaaagatgg aaggcttcgg 1740

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55 gtgaatgatc aactgatacg agtaaatggc gaatccctgt tgggcagac aaaccaggat 1800
 56 gccatggaaa ccctaagaag gtctatgtct actgaaggca ataaacgagg aatgatccag 1860
 57 cttattgtt caaggagaat aagcaagtgc aatgagctga agtcacctgg gagccccct 1920
 58 ggacctgagc tgcccattgc aacagcggtt gatgatagag aacgaagaat ttcccatcc 1980
 59 ctctacagtgg ggttgggg gcttgatgaa tccccaaagca gaaaatgtgc ctcagtagg 2040
 60 ataatgggt aataccagct gtcccctaca gtgaatatgc cccaagatga cactgtcatt 2100
 61 atagaagatg acaggttgc aatgtttccct ccacatctct ctgaccagtc ctctccagc 2160
 62 tccccatgtatg atgtggggtt tggacggca gatgctggta ctggggccaa ggctgcaatc 2220
 63 agtatttcg ccgactgctc tttgagtccaa gatgttgc cagttcttgc tttcaacgca 2280
 64 gaaggatttgc gacgtcagat agctgacgag actaaactca atacagtgg a tgaccagaaa 2340
 65 gcaggttctc ccagcagaga tgggttcct tccctgggtc tgaagaagtc aagctcggt 2400
 66 qagagtctgc agaccgcagt tgccgagggtg actttgaatg gggatattcc tttccatcg 2460
 67 ccacggccgc ggataatcag aggcaggggg tgcaatgaga gttcagagc tgccatcgac 2520
 68 aaatctttagt ataaaccgc ggttagatgat gatgatgagg gcatggagac ctggaaagaa 2580
 69 gacacagaag aaagttcaag atcaggggaga gagtctgtat ccacagccag tgatcagcct 2640
 70 tccccactctc tggagagaca aatgaatggc aaccaagaga aagggtataa gactgataga 2700
 71 aaaaaggata aaactggaaa agaaaaagaag aaagatagag ataaggagaa ggataaaatg 2760
 72 aaagccaaga agggaatgct gaaaggctt gggagacatgt tcagggttgg caaacatcga 2820
 73 aaagatgaca agattggaaa aacgggtaaa ataaaaatac aagaatcct tacatcagaa 2880
 74 gaggagagga tacgaatgaa gcaggagcag gagaggattc aagccaaaac tcgagaattt 2940
 75 agggAACGAC aagctcgaga gctgtactat gctgaaattc aagattttca tcggacattt 3000
 76 ggctgtatg atgagttat gtatgggggatgttctt atgaaggttc catggctctc 3060
 77 aacgcttagac ctcagagccc acgagaaggcatatgatgg atgctttgtatggccaaatg 3120
 78 aagaAGCCGC ggaattccaa accctcacct gtagacagta acagatcaac tcctagcaat 3180
 79 catgatcgga tacagctctc gaggcaagaa tttcagcaag caaagcaaga tgaagatgt 3240
 80 gaagatcgctc ggcggaccta tagttttgag caaccctggc cgaacgcacg gccggcgacg 3300
 81 cagagcgggc gacactcggt gtccgtggag gtgcagatgc agccgcacgc gcaggaggag 3360
 82 cgcgagagct cccagcaggc ccagcgccag tacagctctc tgcctcgccaa aagcaggaaa 3420
 83 aatgccagct cggctctccca ggactcttgg gaggcact acgtccctgg ggaaggcttc 3480
 84 cagagtgc aagagaaccc caggtactcc agtaccaag gtcggcggacg cggctacctg 3540
 85 ggaggacatg gcttcaacgc cagggtcatg ctggaaactc aggagctct tcggccaggaa 3600
 86 cagaggcgga aggagcagca gatgaagaag cagcctcctt ccggggggcc cagcaactat 3660
 87 gactcgata agaaagtccaa ggacccctgt tacgcccctc ccaaggggcc ctccggcaa 3720
 88 gatgtccccc cctcccttc tcaggttgcg aggctgaaca gacttcagac tcctgagaaa 3780
 89 gggaggccct tctattcctg a 3801
 91 <210> SEQ ID NO: 2
 92 <211> LENGTH: 1266
 93 <212> TYPE: PRT
 94 <213> ORGANISM: Homo sapiens
 95 <400> SEQUENCE: 2
 96 Met Lys Val Thr Val Cys Phe Gly Arg Thr Arg Val Val Val Pro Cys
 97 1 5 10 15
 98 Gly Asp Gly His Met Lys Val Phe Ser Leu Ile Gln Gln Ala Val Thr
 99 20 25 30
 100 Arg Tyr Arg Lys Ala Ile Ala Lys Asp Pro Asn Tyr Trp Ile Gln Val
 101 35 40 45
 102 His Arg Leu Glu His Gly Asp Gly Gly Ile Leu Asp Leu Asp Asp Ile
 103 50 55 60
 104 Leu Cys Asp Val Ala Asp Asp Lys Asp Arg Leu Val Ala Val Phe Asp

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106	65	70	75	80												
107	Glu	Gln	Asp	Pro	His	His	Gly	Gly	Asp	Gly	Thr	Ser	Ala	Ser	Ser	Thr
108																95
109	Gly	Thr	Gln	Ser	Pro	Glu	Ile	Phe	Gly	Ser	Glu	Leu	Gly	Thr	Asn	Asn
110																110
111	Val	Ser	Ala	Phe	Gln	Pro	Tyr	Gln	Ala	Thr	Ser	Glu	Ile	Glu	Val	Thr
112																125
113	Pro	Ser	Val	Leu	Arg	Ala	Asn	Met	Pro	Leu	His	Val	Arg	Arg	Ser	Ser
114																140
115	Asp	Pro	Ala	Leu	Ile	Gly	Leu	Ser	Thr	Ser	Val	Ser	Asp	Ser	Asn	Phe
116	145															160
117	Ser	Ser	Glu	Glu	Pro	Ser	Arg	Lys	Asn	Pro	Thr	Arg	Trp	Ser	Thr	Thr
118																175
119	Ala	Gly	Phe	Leu	Lys	Gln	Asn	Thr	Ala	Gly	Ser	Pro	Lys	Thr	Cys	Asp
120																190
121	Arg	Lys	Asp	Glu	Asp	Gly	Thr	Glu	Glu	Asp	Asn	Ser	Arg	Val	Glu	Pro
122																205
123	Val	Gly	His	Ala	Asp	Thr	Gly	Leu	Glu	His	Ile	Pro	Asn	Phe	Ser	Leu
124																220
125	Asp	Asp	Met	Val	Lys	Leu	Val	Glu	Val	Pro	Asn	Asp	Gly	Gly	Pro	Leu
126	225															240
127	Gly	Ile	His	Val	Val	Pro	Phe	Ser	Ala	Arg	Gly	Gly	Arg	Thr	Leu	Gly
128																255
129	Leu	Leu	Val	Lys	Arg	Leu	Glu	Lys	Gly	Gly	Lys	Ala	Glu	His	Glu	Asn
130																270
131	Leu	Phe	Arg	Glu	Asn	Asp	Cys	Ile	Val	Arg	Ile	Asn	Asp	Gly	Asp	Leu
132																285
133	Arg	Asn	Arg	Arg	Phe	Glu	Gln	Ala	Gln	His	Met	Phe	Arg	Gln	Ala	Met
134																300
135	Arg	Thr	Pro	Ile	Ile	Trp	Phe	His	Val	Val	Pro	Ala	Ala	Asn	Lys	Glu
136	305															320
137	Gln	Tyr	Glu	Gln	Leu	Ser	Gln	Ser	Glu	Lys	Asn	Asn	Tyr	Tyr	Ser	Ser
138																335
139	Arg	Phe	Ser	Pro	Asp	Ser	Gln	Tyr	Ile	Asp	Asn	Arg	Ser	Val	Asn	Ser
140																350
141	Ala	Gly	Leu	His	Thr	Val	Gln	Arg	Ala	Pro	Arg	Leu	Asn	His	Pro	Pro
142																365
143	Glu	Gln	Ile	Asp	Ser	His	Ser	Arg	Leu	Pro	His	Ser	Ala	His	Pro	Ser
144																380
145	Gly	Lys	Pro	Pro	Ser	Ala	Pro	Ala	Ser	Ala	Pro	Gln	Asn	Val	Phe	Ser
146	385															400
147	Thr	Thr	Val	Ser	Ser	Gly	Tyr	Asn	Thr	Lys	Lys	Ile	Gly	Lys	Arg	Leu
148																415
149	Asn	Ile	Gln	Leu	Lys	Lys	Gly	Thr	Glu	Gly	Leu	Gly	Phe	Ser	Ile	Thr
150																430
151	Ser	Arg	Asp	Val	Thr	Ile	Gly	Gly	Ser	Ala	Pro	Ile	Tyr	Val	Lys	Asn
152																445
153	Ile	Leu	Pro	Arg	Gly	Ala	Ala	Ile	Gln	Asp	Gly	Arg	Leu	Lys	Ala	Gly
154																460

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155 Asp Arg Leu Ile Glu Val Asn Gly Val Asp Leu Val Gly Lys Ser Gln
156 465 470 475 480
157 Glu Glu Val Val Ser Leu Leu Arg Ser Thr Lys Met Glu Gly Thr Val
158 485 490 495
159 Ser Leu Leu Val Phe Arg Gln Glu Asp Ala Phe His Pro Arg Glu Leu
160 500 505 510
161 Lys Ala Glu Asp Glu Asp Ile Val Leu Thr Pro Asp Gly Thr Arg Glu
162 515 520 525
163 Phe Leu Thr Phe Glu Val Pro Leu Asn Asp Ser Gly Ser Ala Gly Leu
164 530 535 540
165 Gly Val Ser Val Lys Gly Asn Arg Ser Lys Glu Asn His Ala Asp Leu
166 545 550 555 560
167 Gly Ile Phe Val Lys Ser Ile Ile Asn Gly Gly Ala Ala Ser Lys Asp
168 565 570 575
169 Gly Arg Leu Arg Val Asn Asp Gln Leu Ile Ala Val Asn Gly Glu Ser
170 580 585 590
171 Leu Leu Gly Lys Thr Asn Gln Asp Ala Met Glu Thr Leu Arg Arg Ser
172 595 600 605
173 Met Ser Thr Glu Gly Asn Lys Arg Gly Met Ile Gln Leu Ile Val Ala
174 610 615 620
175 Arg Arg Ile Ser Lys Cys Asn Glu Leu Lys Ser Pro Gly Ser Pro Pro
176 625 630 635 640
177 Gly Pro Glu Leu Pro Ile Glu Thr Ala Leu Asp Asp Arg Glu Arg Arg
178 645 650 655
179 Ile Ser His Ser Leu Tyr Ser Gly Ile Glu Gly Leu Asp Glu Ser Pro
180 660 665 670
181 Ser Arg Asn Ala Ala Leu Ser Arg Ile Met Gly Lys Tyr Gln Leu Ser
182 675 680 685
183 Pro Thr Val Asn Met Pro Gln Asp Asp Thr Val Ile Ile Glu Asp Asp
184 690 695 700
185 Arg Leu Pro Val Leu Pro Pro His Leu Ser Asp Gln Ser Ser Ser Ser
186 705 710 715 720
187 Ser His Asp Asp Val Gly Phe Val Thr Ala Asp Ala Gly Thr Trp Ala
188 725 730 735
189 Lys Ala Ala Ile Ser Asp Ser Ala Asp Cys Ser Leu Ser Pro Asp Val
190 740 745 750
191 Asp Pro Val Leu Ala Phe Gln Arg Glu Gly Phe Gly Arg Gln Ile Ala
192 755 760 765
193 Asp Glu Thr Lys Leu Asn Thr Val Asp Asp Gln Lys Ala Gly Ser Pro
194 770 775 780
195 Ser Arg Asp Val Gly Pro Ser Leu Gly Leu Lys Lys Ser Ser Ser Leu
196 785 790 795 800
197 Glu Ser Leu Gln Thr Ala Val Ala Glu Val Thr Leu Asn Gly Asp Ile
198 805 810 815
199 Pro Phe His Arg Pro Arg Pro Arg Ile Ile Arg Gly Arg Gly Cys Asn
200 820 825 830
201 Glu Ser Phe Arg Ala Ala Ile Asp Lys Ser Tyr Asp Lys Pro Ala Val
202 835 840 845
203 Asp Asp Asp Glu Gly Met Glu Thr Leu Glu Asp Thr Glu Glu

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204	850	855	860
205	Ser Ser Arg Ser Gly Arg Glu Ser Val Ser Thr Ala Ser Asp Gln Pro		
206	865	870	875
207	Ser His Ser Leu Glu Arg Gln Met Asn Gly Asn Gln Glu Lys Gly Asp		880
208	885	890	895
209	Lys Thr Asp Arg Lys Lys Asp Lys Thr Gly Lys Glu Lys Lys Lys Asp		
210	900	905	910
211	Arg Asp Lys Glu Lys Asp Lys Met Lys Ala Lys Lys Gly Met Leu Lys		
212	915	920	925
213	Gly Leu Gly Asp Met Phe Arg Phe Gly Lys His Arg Lys Asp Asp Lys		
214	930	935	940
215	Ile Glu Lys Thr Gly Lys Ile Lys Gln Glu Ser Phe Thr Ser Glu		
216	945	950	955
217	Glu Glu Arg Ile Arg Met Lys Gln Glu Gln Glu Arg Ile Gln Ala Lys		960
218	965	970	975
219	Thr Arg Glu Phe Arg Glu Arg Gln Ala Arg Glu Arg Asp Tyr Ala Glu		
220	980	985	990
221	Ile Gln Asp Phe His Arg Thr Phe Gly Cys Asp Asp Glu Leu Met Tyr		
222	995	1000	1005
223	Gly Gly Val Ser Ser Tyr Glu Gly Ser Met Ala Leu Asn Ala Arg Pro		
224	1010	1015	1020
225	Gln Ser Pro Arg Glu Gly His Met Met Asp Ala Leu Tyr Ala Gln Val		
226	1025	1030	1035
227	Lys Lys Pro Arg Asn Ser Lys Pro Ser Pro Val Asp Ser Asn Arg Ser		1040
228	1045	1050	1055
229	Thr Pro Ser Asn His Asp Arg Ile Gln Arg Leu Arg Gln Glu Phe Gln		
230	1060	1065	1070
231	Gln Ala Lys Gln Asp Glu Asp Val Glu Asp Arg Arg Arg Thr Tyr Ser		
232	1075	1080	1085
233	Phe Glu Gln Pro Trp Pro Asn Ala Arg Pro Ala Thr Gln Ser Gly Arg		
234	1090	1095	1100
235	His Ser Val Ser Val Glu Val Gln Met Gln Arg Gln Arg Gln Glu Glu		
236	1105	1110	1115
237	Arg Glu Ser Ser Gln Gln Ala Gln Arg Gln Tyr Ser Ser Leu Pro Arg		1120
238	1125	1130	1135
239	Gln Ser Arg Lys Asn Ala Ser Ser Val Ser Gln Asp Ser Trp Glu Gln		
240	1140	1145	1150
241	Asn Tyr Ser Pro Gly Glu Gly Phe Gln Ser Ala Lys Glu Asn Pro Arg		
242	1155	1160	1165
243	Tyr Ser Ser Tyr Gln Gly Ser Arg Asn Gly Tyr Leu Gly Gly His Gly		
244	1170	1175	1180
245	Phe Asn Ala Arg Val Met Leu Glu Thr Gln Glu Leu Leu Arg Gln Glu		
246	1185	1190	1195
247	Gln Arg Arg Lys Glu Gln Gln Met Lys Lys Gln Pro Pro Ser Glu Gly		1200
248	1205	1210	1215
249	Pro Ser Asn Tyr Asp Ser Tyr Lys Lys Val Gln Asp Pro Ser Tyr Ala		
250	1220	1225	1230
251	Pro Pro Lys Gly Pro Phe Arg Gln Asp Val Pro Pro Ser Pro Ser Gln		
252	1235	1240	1245

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12